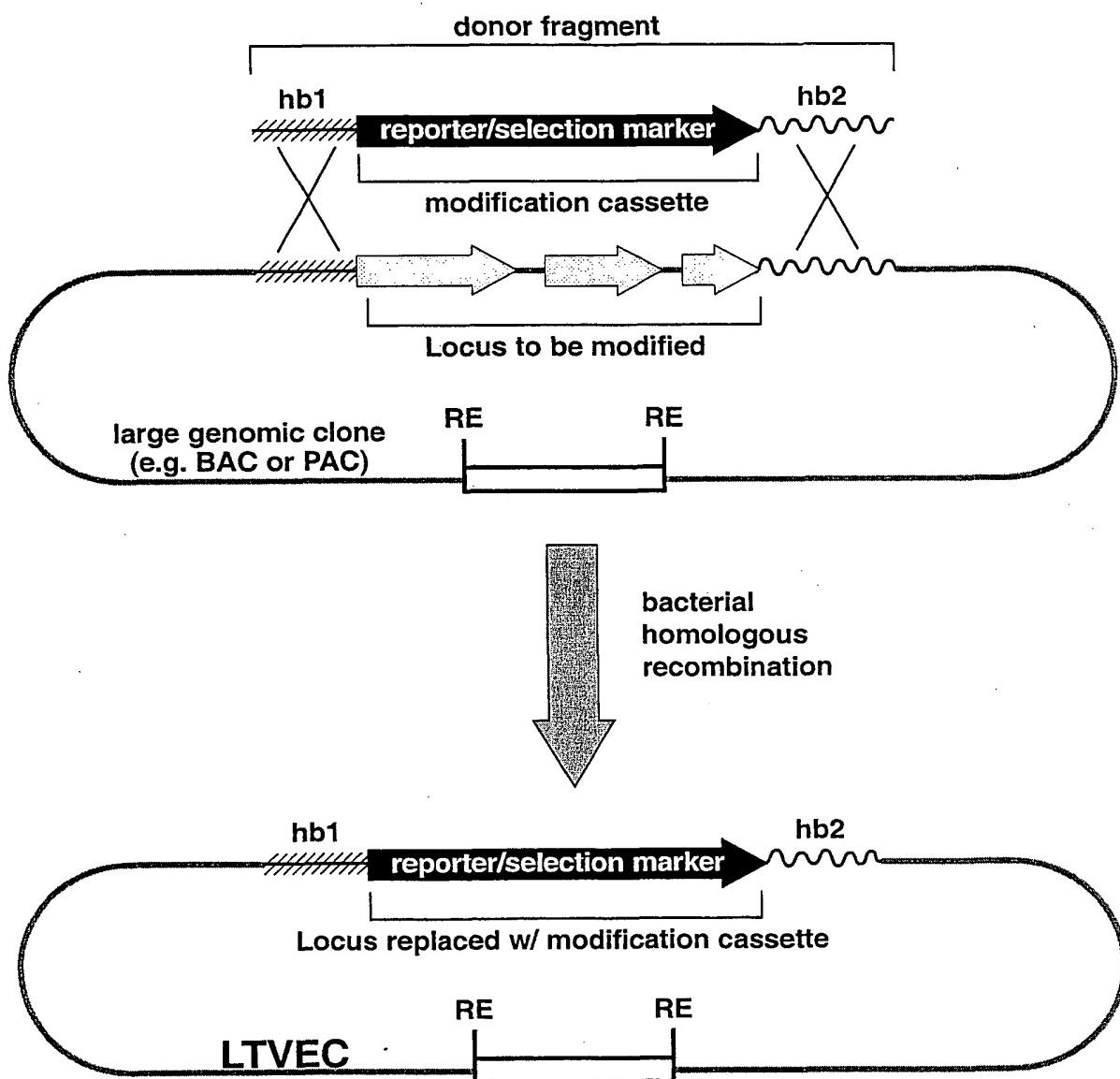
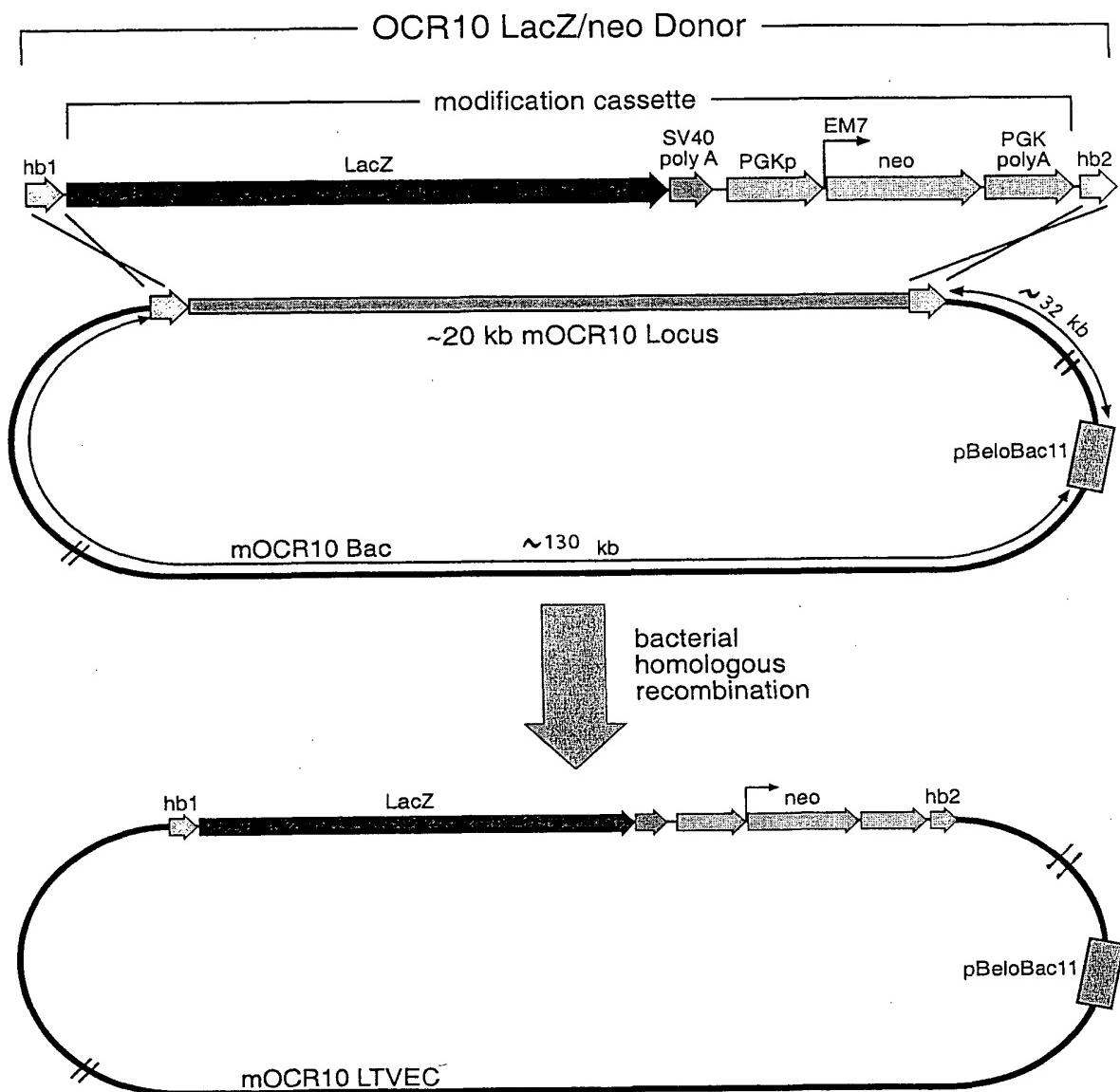


1/7  
Figure 1



2/7  
Figure 2



Att. Docket No. REG 780D  
Inventors: Andrew J. Murphy, et al.  
Title: METHODS OF MODIFYING  
EUKARYOTIC CELLS

3/7

FIGURE 3A

10 20 30 40 50 60  
CCCCGGGCTT CCTGTTCTAA TAAGAATACC TCCTAGGTCC CCCATGGGCT AACCTCATCT  
GGGGCCCCGAA GGACAAGATT ATTCTTATGG AGGATCCAGG GGGTACCCGA TTGGAGTAGA

70 80 90 100 110 120  
TTGGTACTCA ACAGGGGTCT TCTTTATGAG CTTCGGACCA GCTCTTTGA TGTGGCAGGG  
AACCATGAGT TGTCCCCAGA AGAAATACTC GAAGCCTGGT CGAGAAAAC ACTACCGTC

130 140 150 160 170 180  
ACTGACCCCTG GGTGGGGAAG CCACTCAGTG CATGACCCCCA GCTGGTTCAC CACATATACC  
TGACTGGGAC CCACCCCTTC GGTGAGTCAC GTACTGGGGT CGACCAAGTG GTGTATATGG

190 200 210 220 230  
ACATACTTTT CTTGCAGGTC TGGGACACAG C ATG CCC CGG GGC CCA GTG GCT GCC  
TGTATGAAAAA GAACGTCCAG ACCCTGTGTC G TAC GGG GCC CCG GGT CAC CGA CGG  
Met Pro Arg Gly Pro Val Ala Ala>

240 250 260 270 280  
TTA CTC CTG CTG ATT CTC CAT GGA GCT TGG AGC TGC CTG GAC CTC ACT  
AAT GAG GAC GAC TAA GAG GTA CCT CGA ACC TCG ACG GAC CTG GAG TGA  
Leu Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr>

290 300 310 320 330  
TGC TAC ACT GAC TAC CTC TGG ACC ATC ACC TGT GTC CTG GAG ACA CGG  
ACG ATG TGA CTG ATG GAG ACC TGG TAG TGG ACA CAG GAC CTC TGT GCC  
Cys Tyr Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg>

340 350 360 370  
AGC CCC AAC CCC AGC ATA CTC AGT CTC ACC TGG CAA GAT GAA TAT GAG  
TCG GGG TTG GGG TCG TAT GAG TCA GAG TGG ACC GTT CTA CTT ATA CTC  
Ser Pro Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu>

380 390 400 410 420  
GAA CTT CAG GAC CAA GAG ACC TTC TGC AGC CTA CAC AAG TCT GGC CAC  
CTT GAA GTC CTG GTT CTC TGG AAG ACG TCG GAT GTG TTC AGA CCG GTG  
Glu Leu Gln Asp Gln Glu Thr Phe Cys Ser Leu His Lys Ser Gly His>

430 440 450 460 470  
AAC ACC ACA CAT ATA TGG TAC ACG TGC CAT ATG CGC TTG TCT CAA TTC  
TTG TGG TGT GTA TAT ACC ATG TGC ACG GTA TAC GCG AAC AGA GTT AAG  
Asn Thr Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe>

480 490 500 510 520  
CTG TCC GAT GAA GTT TTC ATT GTC AAC GTG ACG GAC CAG TCT GGC AAC  
GAC AGG CTA CTT CAA AAG TAA CAG TTG CAC TGC CTG GTC AGA CCG TTG  
Leu Ser Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn>

530 540 550 560 570  
AAC TCC CAA GAG TGT GGC AGC TTT GTC CTG GCT GAG AGC ATC AAG CCA  
TTG AGG GTT CTC ACA CCG TCG AAA CAG GAC CGA CTC TCG TAG TTC GGT  
Asn Ser Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro>

Att. Docket No. REG 780D  
Inventors: Andrew J. Murphy, et al.  
Title: METHODS OF MODIFYING  
EUKARYOTIC CELLS

4/7

FIGURE 3B

580            590            600            610  
GCT CCC CCC TTG AAC GTG ACT GTG GCC TTC TCA GGA CGC TAT GAT ATC  
CGA GGG GGG AAC TTG CAC TGA CAC CGG AAG AGT CCT GCG ATA CTA TAG  
Ala Pro Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile>  
  
620            630            640            650            660  
TCC TGG GAC TCA GCT TAT GAC GAA CCC TCC AAC TAC GTG CTG AGA GGC  
AGG ACC CTG AGT CGA ATA CTG CTT GGG AGG TTG ATG CAC GAC TCT CCG  
Ser Trp Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly>  
  
670            680            690            700            710  
AAG CTA CAA TAT GAG CTG CAG TAT CGG AAC CTC AGA GAC CCC TAT GCT  
TTC GAT GTT ATA CTC GAC GTC ATA GCC TTG GAG TCT CTG GGG ATA CGA  
Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala>  
  
720            730            740            750            760  
GTG AGG CCG GTG ACC AAG CTG ATC TCA GTG GAC TCA AGA AAC GTC TCT  
CAC TCC GGC CAC TGG TTC GAC TAG AGT CAC CTG AGT TCT TTG CAG AGA  
Val Arg Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser>  
  
770            780            790            800            810  
CTT CTC CCT GAA GAG TTC CAC AAA GAT TCT AGC TAC CAG CTG CAG ATG  
GAA GAG GGA CTT CTC AAG GTG TTT CTA AGA TCG ATG GTC GAC GTC TAC  
Leu Leu Pro Glu Glu His Lys Asp Ser Ser Tyr Gln Leu Gln Met>  
  
820            830            840            850  
CGG GCA GCG CCT CAG CCA GCC ACT TCA TTC AGG GGG ACC TGG AGT GAG  
GCC CGT CGC GGA GTC GGT CCG TGA AGT AAG TCC CCC TGG ACC TCA CTC  
Arg Ala Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu>  
  
860            870            880            890            900  
TGG AGT GAC CCC GTC ATC TTT CAG ACC CAG GCT GGG GAG CCC GAG GCA  
ACC TCA CTG GGG CAG TAG AAA GTC TGG GTC CGA CCC CTC GGG CTC CGT  
Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala>  
  
910            920            930            940            950  
GGC TGG GAC CCT CAC ATG CTG CTG CTC CTG GCT GTC TTG ATC ATT GTC  
CCG ACC CTG GGA GTG TAC GAC GAC GAG GAC CGA CAG AAC TAG TAA CAG  
Gly Trp Asp Pro His Met Leu Leu Leu Ala Val Leu Ile Ile Val>  
  
960            970            980            990            1000  
CTG GTT TTC ATG GGT CTG AAG ATC CAC CTG CCT TGG AGG CTA TGG AAA  
GAC CAA AAG TAC CCA GAC TTC TAG GTG GAC GGA ACC TCC GAT ACC TTT  
Leu Val Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys>  
  
1010           1020           1030           1040           1050  
AAG ATA TGG GCA CCA GTG CCC ACC CCT GAG AGT TTC TCC CAG CCC CTG  
TTC TAT ACC CGT GGT CAC GGG TGG GGA CTC TCA AAG AAG GTC GGG GAC  
Lys Ile Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu>

Att. Docket No. REG 780D  
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Title: METHODS OF MODIFYING  
EUKARYOTIC CELLS

5/7

FIGURE 3C

1060            1070            1080            1090  
TAC AGG GAG CAC AGC GGG AAC TTC AAG AAA TGG GTT AAT ACC CCT TTC  
ATG TCC CTC GTG TCG CCC TTG AAG TTC TTT ACC CAA TTA TGG GGA AAG  
Tyr Arg Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe>  
  
1100            1110            1120            1130            1140  
ACG GCC TCC AGC ATA GAG TTG GTG CCA CAG AGT TCC ACA ACA ACA TCA  
TGC CGG AGG TCG TAT CTC AAC CAC GGT GTC TCA AGG TGT TGT TGT AGT  
Thr Ala Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Ser>  
  
1150            1160            1170            1180            1190  
GCC TTA CAT CTG TCA TTG TAT CCA GCC AAG GAG AAG AAG TTC CCG GGG  
CGG AAT GTA GAC AGT AAC ATA GGT CGG TTC CTC TTC TTC AAG GGC CCC  
Ala Leu His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly>  
  
1200            1210            1220            1230            1240  
CTG CCG GGT CTG GAA GAG CAA CTG GAG TGT GAT GGA ATG TCT GAG CCT  
GAC GGC CCA GAC CTT CTC GTT GAC CTC ACA CTA CCT TAC AGA CTC GGA  
Leu Pro Gly Leu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro>  
  
1250            1260            1270            1280            1290  
GGT CAC TGG TGC ATA ATC CCC TTG GCA GCT GGC CAA GCG GTC TCA GCC  
CCA GTG ACC ACG TAT TAG GGG AAC CGT CGA CCG GTT CGC CAG AGT CGG  
Gly His Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala>  
  
1300            1310            1320            1330  
TAC AGT GAG GAG AGA GAC CGG CCA TAT GGT CTG GTG TCC ATT GAC ACA  
ATG TCA CTC CTC TCT CTG GCC GGT ATA CCA GAC CAC AGG TAA CTG TGT  
Tyr Ser Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr>  
  
1340            1350            1360            1370            1380  
GTG ACT GTG GGA GAT GCA GAG GGC CTG TGT GTC TGG CCC TGT AGC TGT  
CAC TGA CAC CCT CTA CGT CTC CCG GAC ACA CAG ACC GGG ACA TCG ACA  
Val Thr Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys>  
  
1390            1400            1410            1420            1430  
GAG GAT GAT GGC TAT CCA GCC ATG AAC CTG GAT GCT GGC AGA GAG TCT  
CTC CTA CTA CCG ATA GGT CGG TAC TTG GAC CTA CGA CCG TCT CTC AGA  
Glu Asp Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser>  
  
1440            1450            1460            1470            1480  
GGT CCT AAT TCA GAG GAT CTG CTC TTG GTC ACA GAC CCT GCT TTT CTG  
CCA GGA TTA AGT CTC CTA GAC GAG AAC CAG TGT CTG GGA CGA AAA GAC  
Gly Pro Asn Ser Glu Asp Leu Leu Val Thr Asp Pro Ala Phe Leu>  
  
1490            1500            1510            1520            1530  
TCT TGT GGC TGT GTC TCA GGT AGT GGT CTC AGG CTT GGG GGC TCC CCA  
AGA ACA CCG ACA CAG AGT CCA TCA CCA GAG TCC GAA CCC CCG AGG GGT  
Ser Cys Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro>

Att. Docket No. REG 780D  
Inventors: Andrew J. Murphy, et al.  
Title: METHODS OF MODIFYING  
EUKARYOTIC CELLS

6/7

Figure 3D

1540            1550            1560            1570  
GGC AGC CTA CTG GAC AGG TTG AGG CTG TCA TTT GCA AAG GAA GGG GAC  
CCG TCG GAT GAC CTG TCC AAC TCC GAC AGT AAA CGT TTC CTT CCC CTG  
Gly Ser Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp>  
  
1580            1590            1600            1610            1620  
TGG ACA GCA GAC CCA ACC TGG AGA ACT GGG TCC CCA GGA GGG GGC TCT  
ACC TGT CGT CTG GGT TGG ACC TCT TGA CCC AGG GGT CCT CCC CCG AGA  
Trp Thr Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Ser>  
  
1630            1640            1650            1660            1670  
GAG AGT GAA GCA GGT TCC CCC CCT GGT CTG GAC ATG GAC ACA TTT GAC  
CTC TCA CTT CGT CCA AGG GGG GGA CCA GAC CTG TAC CTG TGT AAA CTG  
Glu Ser Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp>  
  
1680            1690            1700            1710            1720  
AGT GGC TTT GCA GGT TCA GAC TGT GGC AGC CCC GTG GAG ACT GAT GAA  
TCA CCG AAA CGT CCA AGT CTG ACA CCG TCG GGG CAC CTC TGA CTA CTT  
Ser Gly Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu>  
  
1730            1740            1750            1760            1770  
GGA CCC CCT CGA AGC TAT CTC CGC CAG TGG GTG GTC AGG ACC CCT CCA  
CCT GGG GGA GCT TCG ATA GAG GCG GTC ACC CAC CAG TCC TGG GGA GGT  
Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro>  
  
1780            1790            1800  
CCT GTG GAC AGT GGA GCC CAG AGC AGC TAG  
GGA CAC CTG TCA CCT CGG GTC TCG TCG ATC  
Pro Val Asp Ser Gly Ala Gln Ser Ser \*\*\*>

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Figure 4A Human Ig heavy chain locus (total length  $\approx$ 1Mb, not drawn to scale):

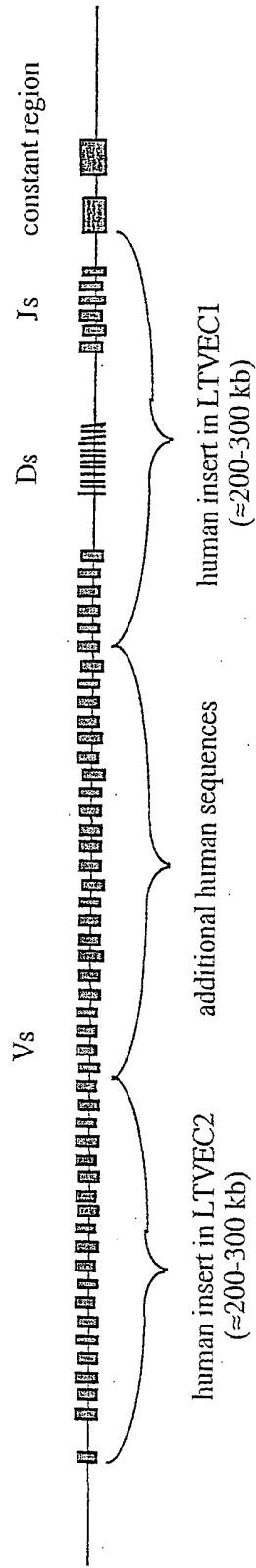


Figure 4B Mouse Ig heavy chain locus (total length  $\approx$ 1Mb, not drawn to scale):

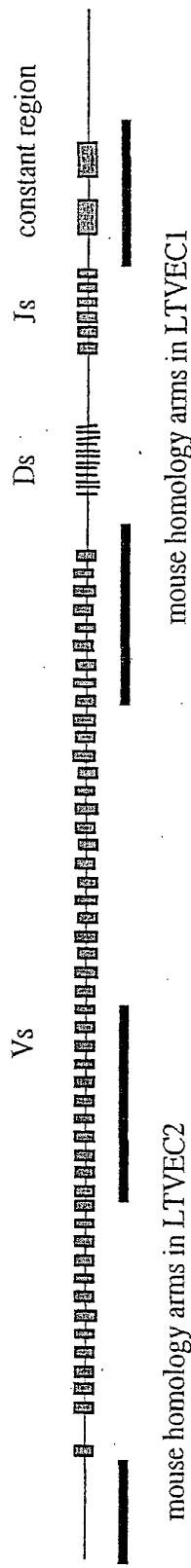


Figure 4C LTVEC2:

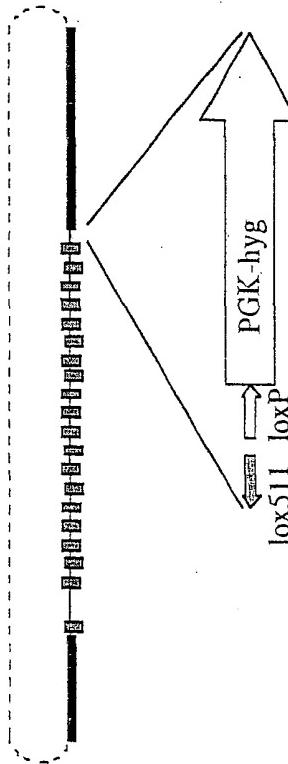


Figure 4d LTVEC1:

